

CLAIMS

1. Nucleotides encoding the full length or part of the nucleocapsid (NP) protein of Newcastle disease virus (NDV).

2. The nucleotides as claimed in claim 1 characterised in that it has the following nucleotide sequence:

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      10      20      30      40      50      60
ATGTCTTCGG TATTCGATGA ATACGAGCAG CTCCTCGCTG CTCAGACTCG CCCCAATGGA

      70      80      90     100     110     120
GCTCACGGAG GGGGAGAGAG AGGGAGCACT TTAAGAGTTG AGGTCCCAGT ATTCACTCTT

10      130     140     150     160     170     180
AACAGTGACG ATCCAGAAGA TAGATGGART TTTGCGGTAT TCTGTCTTCG GATTGCTGTT

      190     200     210     220     230     240
AGCGAGGACG CCAACAACC GCTCAGGCAA GGTGCTCTCA TATCCCTCCT GTGCTCCCAT

15      250     260     270     280     290     300
TCTCAAGTGA TGAGGAACCA TGTTCGCCCT GCAGGAAAAC AGAATGAGG TACACTGACT

      310     320     330     340     350     360
GTTCTTGAGA TCGATGGTTT TACCAGCAGC GTGCCTCAGT TCAACAACAG GAGTGGGGTG

      370     380     390     400     410     420
TCTGAGGAGA GAGCACAGAG ATTCATGGTG ATAGCAGGGT CTCTCCCTCG GCGGTGCAGT

20      430     440     450     460     470     480
AACGGTACTC CGTTCGTCAC GGCTGGGGTT GAAGATGATG CACCAGAAGA TATCACTGAT

      490     500     510     520     530     540
ACTCTGGAAA GAATCCTGTC TATCCAGGCT CAGGTATGGG TCACAGTAGC GAAGGCCATG

      550     560     570     580     590     600
25 ACTGCATATG AGACAGCAGA TGAGTCGGAA ACAAGAAGAA TCAATAAGTA CATGCAGCAA

      610     620     630     640     650     660
GGCAGAGTCC AGAAGAAGTA CATCCTCCAC CCTGTATGCA GGAGTGCAAT TCAACTCACA

      670     680     690     700     710     720
ATCAGACATT CTCGCGCAGT CCGCATTTC TTAGTTAGCG AGCTTAAGAG AGGCCCGCAAT

30      730     740     750     760     770     780
ACGGCAGGTG GGAGCTCCAC GTATTACAAC TTAGTAGGGG ATGTAGACTC ATACATCAGG

      790     800     810     820     830     840
AACACCGGAC TTAAGTGCAT CTTCCTTACA CTCAAAATATG GAATTAATAC CAAGACATCA

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	850	860	870	880	890	900
	GCCCTAGCAC	TCAGCAGCCT	CACAGGCGAT	ATCCAAAAGA	TGAAGCAGCT	CATGCGTTTA
	910	920	930	940	950	960
	TATCGGATGA	AGGGAGAAAA	TGCGCCGTAC	ATGCATTGCT	TAGGTGACAG	TGATCAGATG
5	970	980	990	1000	1010	1020
	AGCTTTGCAC	CGGCTGAGTA	TGCACAGCTT	TATTCTTTTG	CCATGGGCAT	GGCATCAGTC
	1030	1040	1050	1060	1070	1080
	TTAGATAAAG	GAAGTGGCAA	ATACCAATTC	GCCAGAGACT	TCATGAGCAC	ATCATTCTGG
10	1090	1100	1110	1120	1130	1140
	AGACTCGGGG	TGGAGTATGC	TCAGGCTCAG	GGGAGTAGCA	TCAACGAAGA	CATGGCTGCT
	1150	1160	1170	1180	1190	1200
	GAGCTAAAC	TAACCCCGGC	AGCAAGAAGG	GGCCTGGCAG	CTGCTGCCCA	ACGAGTGTCT
	1210	1220	1230	1240	1250	1260
	GAGGAAACTG	GCAGCGTGGA	TATTCCTACT	CAACAAGCCG	GGGTCTCTAC	TGGGCTCAGC
15	1270	1280	1290	1300	1310	1320
	GATGGAGGCC	CCCAGCCCTC	TCAGGGTGGA	TCGAACAAGT	CGCAAGGGCA	ACCGATGCTC
	1330	1340	1350	1360	1370	1380
	GGAGATGGGG	AGACCCAATT	CTTGGATTG	ATGAGAGCAG	TGGCGAACAG	CATGCGAGAA
20	1390	1400	1410	1420	1430	1440
	GCGCCAACCT	CCGCACAGAG	CACCACCACC	CCGGAACCCC	CCCGAGTCCG	CGGGCCATCA
	1450	1460	1470	1480	1490	1500
	CAAGATAACG	ACACCGACTG	GGGGTATTGA

3. Nucleotides encoding the full length or part of the phosphoprotein (P) of Newcastle disease virus (NDV).

25 4. The nucleotides as claimed in claim 3 characterised in that it has the following nucleotide sequence:

	10	20	30	40	50	60
	ATGGCCACCT	TTACAGATGC	GGAGATAGAT	GATATATTTG	AGACCAAGTG	AACTGTCTAT
30	70	80	90	100	110	120
	GACAGCATAA	TTACGGCCCA	GGGTAAATCA	GCAGAGACTG	TCGAAGGAG	CGCAATCCCA
	130	140	150	160	170	180
	CAAGGCAAGA	CCAAAGCGCT	GAGCATAGCA	TGGGAGAAGC	ATGGGAGCAT	CCAACCATCC
	190	200	210	220	230	240
	ACCAGCCAGG	ACAACCCCGA	CCAACAGGAT	AGACCAAGCA	AACAGCTATC	CACACCTGAG
35	250	260	270	280	290	300
	CAGGCGACCC	CACACAACAG	CTCGCCAGCC	ACATCCGCCG	AACCGCTCCC	CACTCAGGCC

	310	320	330	340	350	360
	GCAGGTGAGG	CCGGCGACAC	ACAGTCAAG	ACCGGAGCAA	GCAACTCTCT	TCTGTCTATG
	370	380	390	400	410	420
	CTCGACAAGC	TGAGCAATAA	ACCATCTAAT	GCTAAAAAGG	GCCCATGGTC	GAGTCCCCAG
5	430	440	450	460	470	480
	GAAGGATATC	ATCAACCTCC	GACCCAACAA	CATGGGGATC	AGCCGAACCG	CGGAACACGC
	490	500	510	520	530	540
	CAGGAGAGCG	TGCGGCACCA	AGCCAAGGCC	GCCCTGGAA	GCCGGGGCAC	AGACGCGAGC
10	550	560	570	580	590	600
	ACAGCATATC	ATGGACAATG	GAAGGAGTCA	CAACTATCAG	CTGGTGCAAC	CCCTCATGTG
	610	620	630	640	650	660
	CTCCAATCAG	GGCAGAGCCA	AGACAGTACT	CCTGTACCTG	TGGATCATGT	CCAGCCACCT
	670	680	690	700	710	720
	GTCGACTTTG	TGCAGGCGAT	GATGACTATG	ATGGAGGCGT	TATCAGAGAA	GGTAAGTAAA
15	730	740	750	760	770	780
	GTCGACTATC	AGCTAGACCT	AGTCTTAAAG	CAGACATCCT	CCATCCCTAT	GATGCGGTCT
	790	800	810	820	830	840
	GAAATCCAAC	AGCTAAAAAC	ATCTGTTGCG	GTCATGGAAG	CTAATTTAGG	CATGATGAAA
20	850	860	870	880	890	900
	ATTCTGGACC	CTGGTTGTGC	TAACATTTC	TCCTTAAGTG	ATCTGCGGGC	AGTCGCCCGG
	910	920	930	940	950	960
	TCCCACCCAG	TTTTAATTTC	AGGCCCGGA	GATCCGTCCC	CCTACGTGAC	ACAAGGGGGT
	970	980	990	1000	1010	1020
	GAGATGACAC	TCAATAAACT	CTCACAACCA	GTACAACACC	CTTCCGAGTT	AATTAATCT
25	1030	1040	1050	1060	1070	1080
	GCCACAGCGG	GCGGACCTGA	TATGGGAGTG	GAAGAAGACA	CTGTCCGTGC	ATTGATCACC
	1090	1100	1110	1120	1130	1140
	TCGCGCCCGA	TGCATCCAAG	CTCCTCAGCT	AAGCTCCTGA	GTAAGCTGGA	TGCAGCGGGG
30	1150	1160	1170	1180	1190	1200
	TCGATTGAAG	AGATCAGAAA	GATCAAGCGC	CTTGCACTAA	ATGGCTAA...

5. The NP protein coded according to claim 1 or claim 2 characterised in that it has the following amino acid sequence:

35	1	M	S	S	V	F	D	E	Y	E	Q	L	L	A	A	Q	T	16
		ATG	TCT	TCC	GTA	TTC	GAT	GAA	TAC	GAG	CAG	CTC	CTC	GCT	GCT	CAG	ACT	
		1			10			20			30			40				
	17	R	P	N	G	A	H	G	G	G	E	R	G	S	T	L	R	32
		CGC	CCC	AAT	GGA	GCT	CAC	GGA	GGG	GGA	GAG	AGA	GGG	AGC	ACT	TTA	AGA	
		50			60			70			80			90				

5	33	V E V P V F T L N S D D P E D R	48
		GTT GAG GTC CCA GTA TTC ACT CTT AAC AGT GAC GAT CCA GAA GAT AGA	
		100 110 120 130 140	
	49	W N F A V F C L R I A V S E D A	64
		TGG AAT TTT GCG GTA TTC TGT CTT CGG ATT GCT GGT AGC GAG GAC GCC	
10	65	N K P L R Q G A L I S L L C S H	80
		AAC AAA CCG CTC AGG CAA GGT GCT CTC ATA TCC CTC CTG TGC TCC CAT	
		200 210 220 230 240	
	81	S Q V M R N H V A L A G K Q N E	96
		TCT CAA GTG ATG AGG AAC CAT GGT GCC CTT GCA GGA AAA CAG AAT GAG	
15	97	A T L T V L E I D G F T S S V P	112
		GCT ACA CTG GCT GTT GAG ATC GAT GGT ATT ACC AGC GTG CCT	
		290 300 310 320 330	
	113	Q F N N R S G V S E E R A Q R F	128
		CAG TTC AAC AAC AGG AGT GGG GTG TCT GAG GAG AGA GCA CAG AGA TTC	
20	129	M V I A G S L P R A C S N G T P	144
		ATG GTG ATA GCA GGG TCT CTC CCT CGG GCG TCG AGT AAC GGT ACT CCG	
		390 400 410 420 430	
	145	F V T A G V E D A P E D I T D	160
		TTC CTG ACG GCT GGG GTT GAA GAT GAT GCA CCA GAA GAT ATC ACT GAT	
25	161	T L E R I L S I Q A Q V W V T V	176
		ACT CTG GAA AGA ATC CTG TCT ATC GAG GCT CAG GTA TGG GTC ACA GTA	
		490 500 510 520	
	177	A K A M T A Y E T A D E S E T R	192
		GCG AAG GCC ATG ACT GCA TAT GAG ACA GCA GAT GAG TCG GAA ACA AGA	
30	193	R I N K Y M Q Q G R V Q K K Y I	208
		AGA ATC AAT AAG TAC ATG CAG CAA GGC AGA GTC CAG AAG AAG TAC ATC	
		580 590 600 610 620	
	209	L H P V C R S A I Q L T I R H S	224
		CTC CAC CCT GTA TGC AGG AGT GCA ATT CAA CTC ACA ATC AGA CAT TCT	
35	225	L A V R I F L V S E L K R G R N	240
		CTG GCA GTC CGC ATT TTC TTA GTT AGC GAG CTT AAG AGA GGC CGC AAT	
		680 690 700 710 720	
	241	T A G G S T Y Y N L V G D V D	256
		ACG GCA GGT GGG AGC TCC ACG TAT TAC AAC TTA GTA GGG GAT GTA GAC	
40	257	S Y I R N T G L T A F F L T L K	272
		TCA TAC ATC AGG AAC ACC GGA CTT ACT GCA TTC TTC CTT ACA CTC AAA	
		770 780 790 800 810	
	273	Y G I N T K T S A L A L S S L T	288
		TAT GGA ATT AAT ACC AAG ACA TCA GCC CTA GCA CTC AGC AGC CTC ACA	
45	289	G D I Q K M K Q L M R L Y R M K	304
		GGC GAT ATC CAA AAG ATG AAG CAG CTC ATG CGT TTA TAT CCG ATG AAG	
		870 880 890 900 910	

5	305	G E N A P Y M T L L G D S D Q M	320
		GGA GAA AAT GCG CCG TAC ATG ACA TTG CTA GGT GAC AGT GAT CAG ATG	
		920 930 940 950 960	
	321	S F A P A E Y A Q L Y S F A M G	336
		AGC TTT GCA CCG GCT GAG TAT GCA CAG CTT TAT TCT TTT GCC ATG GGC	
10		970 980 990 1000	
	337	M A S V L D K G T G K Y Q F A R	352
		ATG GCA TCA GTC TTA GAT AAA GGA ACT GGC AAA TAC CAA TTC GCC AGA	
		1010 1020 1030 1040 1050	
	353	D F M S T S F W R L G V E Y A Q	368
15		GAC TTC ATG AGC ACA TCA TTC TGG AGA CTC GGG GTG GAG TAT GCT CAG	
		1060 1070 1080 1090 1100	
	369	A Q G S S I N E D M A A E L K L	384
		GCT CAG GGG AGT AGC ATC AAC GAA GAC ATG GCT GCT GAG CTA AAA CTA	
		1110 1120 1130 1140 1150	
20	385	T P A A R R G L A A A A Q R V S	400
		ACC CCG GCA GCA AGA AGG GGC CTG GCA GCT GCT GCC CAA CGA GTG TCT	
		1160 1170 1180 1190 1200	
	401	E E T G S V D I P T Q Q A G V L	416
		GAG GAA ACT GGC AGC GTG GAT ATT CCT ACT CAA CAA GCC GGG GTC CTC	
25		1210 1220 1230 1240	
	417	T G L S D G G P R A S Q G G S N	432
		ACT GGG CTC AGC GAT GGA GGC CCC CGA GCC TCT CAG GGT GGA TCG AAC	
		1250 1260 1270 1280 1290	
	433	K S Q G Q P D A G D G E T Q F L	448
30		AAG TCG CAA GGG CAA CCA GAT GCC GGA GAT GGG GAG ACC CAA TTC TTG	
		1300 1310 1320 1330 1340	
	449	D L M R A V A N S M R E A P N S	464
		GAT TTG ATG AGA GCA GTG GCG AAC AGC ATG CGA GAA GCG CCA AAC TCC	
		1350 1360 1370 1380 1390	
35	465	A Q S T T H P E P P P T P G P S	480
		GCA CAG AGC ACC ACC CAC CCG GAA CCC CCC CCG ACT CCC GGG CCA TCC	
		1400 1410 1420 1430 1440	
	481	Q D N D T D W G Y *	490
		CAA GAT AAC GAC ACC GAC TGG GGG TAT TGA	
		1450 1460 1470	

6. The P protein coded according to claim 3 or claim 4 characterised in that it has the following amino acid sequence:

40	1	M A T F T D A E I D D I F E T S	16
		ATG GCC ACC TTT ACA GAT CCG GAG ATA GAT GAT ATA TTT GAG ACC AGT	
45	17	G T V I D S I I T A Q G K S A E	32
		GGA ACT GTC ATT GAC AGC ATA ATT ACG GCC CAG GGT AAA TCA GCA GAG	
		50 60 70 80 90	

5	33	T V G R S A I P Q G K T K A L S	48
		ACT GTC GGA AGG AGC GCA ATC CCA CAA GGC AAG ACC AAA GCG CTG AGC	
		100 110 120 130 140	
10	49	I A W E K H G S I Q P S T S Q D	64
		ATA GCA TGG GAG AAG CAT GGG AGC ATC CAA CCA TCC ACC AGC CAG GAC	
		150 160 170 180 190	
15	65	N P D Q Q D R P D K Q L S T P E	80
		AAC CCC GAC CAA CAG GAT AGA CCA GAC AAA CAG CTA TCC ACA CCT GAG	
		200 210 220 230 240	
20	81	Q A G T P H N S S P A T S A E P L	96
		CAG GCG ACC CCA CAC AAC AGC TCG CCA GCC ACA TCC GCC GAA CCG CTC	
		250 260 270 280 290	
25	97	P T Q A A G E A G D T Q L K T G	112
		CCC ACT CAG GCC GCA GGT GAG GCG GAC ACA CAG CTC AAG CCT GGA	
		290 300 310 320 330	
30	113	A S N S L L S M L D K L S N K P	128
		GCA AGC AAC TCT CTT CTG TCT ATG AAT GAT AGC AAT AAA CCA	
		340 350 360 370 380	
35	129	S N A K K G P W S S P Q E G Y H	144
		TCT AAT GCT AAA AAG GGC CCA TGG TCG AGT CCC CAG GAA GGA TAT CAT	
		390 400 410 420 430	
40	145	Q P P T Q Q H G D Q P N R G N S	160
		CAA CCC CCG ACC CAA CAA CAT GGG GAT CAG CCG AAC CGC GGA AAC AGC	
		440 450 460 470 480	
45	161	Q E R L R H Q A K A A P G S R G	176
		CAG GAG AGG CTG CGG CAC CAA GCC AAG GCC GCC CCT GGA AGC CGG GGC	
		490 500 510 520 530	
50	177	T D A S T A Y H G Q W K E S Q L	192
		ACA GAC GCG AGC ACA GCA TAT CAT GGA CAA TGG AAG GAG TCA CAA CTA	
		530 540 550 560 570	
55	193	S A G A T P H V L Q S G Q S Q D	208
		TCA GCT GGT GCA ACC CCT CAT GTG CTC CAA TCA GGG CAG AGC CAA GAC	
		580 590 600 610 620	
60	209	S T P V P V D H V Q P P V D F V	224
		AGT ACT CCT GTA CCT GTG GAT CAT GTC CAG CCA CCT GTC GAC TTT GTG	
		630 640 650 660 670	
65	225	Q A M M T M M E A L S Q K V S K	240
		CAG GCG ATG ATG ACT ATG GAG GCG TTA TCA CAG AAG GTA AGT AAA	
		680 690 700 710 720	
70	241	V D Y Q L D L V L K Q T S S I P	256
		GTC GAC TAT CAG CTA GAC CTA GTC TTA AAG CAG ACA TCC TCC ATC CCT	
		730 740 750 760 770	
75	257	M M R S E I Q Q L K T S V A V M	272
		ATG ATG CGG TCT GAA ATC CAA CAG CTA AAA ACA TCT GTT GCG GTC ATG	
		770 780 790 800 810	
80	273	E A N L G M M K I L D P G C A N	288
		GAA GCT AAT TTA GGC ATG ATG AAA ATT CTG GAC CCT GGT TGT GCT AAC	
		820 830 840 850 860	
85	289	I S S L S D L R A V A R S H P V	304
		ATT TCA TCC TTA AGT GAT CTG CGG GCA GTC GCC TCC CAC CCA GTT	
		870 880 890 900 910	

305 L I S G P G D P S P Y V T Q G G 320
 TTA ATT TCA GGC CCC GGA GAT CCG TCC CCC TAC GTG ACA CAA GGG GGT
 920 930 940 950 960

321 E M T L N K L S Q P V Q H P S E 336
 GAG ATG ACA CTC AAT AAA CTC TCA CAA CCA GTA CAA CAC CCT TCC GAG
 970 980 990 1000

337 L I K S A T A G G P D M G V E K 352
 TTA ATT AAA TCT GCC ACA GCG GGC GGA CCT GAT ATG GGA GTG GAA AAG
 1010 1020 1030 1040 1050

353 D T V R A L I T S R P M H P S S 368
 GAC ACT GTC CGT GCA TTG ATC ACC TCG CGC CCG ATG CAT CCA AGC TCC
 1060 1070 1080 1090 1100

369 S A K L L S K L D A A G S I E E 384
 TCA GCT AAG CTC CTG AGT AAG CTG GAT GCA GCC GGG TCG ATT GAA GAG
 1110 1120 1130 1140 1150

385 I R K I K R L A L N G * 396
 ATC AGA AAG ATC AAG CGC CTT GCA CTA AAT GGC TAA
 1160 1170 1180

7. A recombinant expression plasmid containing the NDV nucleocapsid gene as claimed in claim 1 or claim 2.

8. A recombinant expression plasmid containing the NDV phosphoprotein gene as claimed in claim 3 or claim 4.

9. The recombinant expression plasmid according to claim 7 which is the expression plasmid pTrcHis2-NP constructed by cloning the NDV nucleocapsid gene of claims 1 or 2 into vector pTrcHis2.

10. The recombinant expression plasmid according to claim 8 which is the expression plasmid pTrcHis2-P constructed by cloning the NDV phosphoprotein gene of claims 3 or 4 into vector pTrcHis2.

11. A transformed *Escherichia coli* with the recombinant expression plasmid according to claim 7 or claim 9.

12. A transformed *Escherichia coli* with the recombinant expression plasmid according to claim 8 or claim 10.

13. The transformed microorganism according to claim 11, which is the transformed *E. coli* TOP10 (pTrcHis2-NP) produced by introducing the recombinant expression plasmid of claim 7 or claim 9 into *E. coli* TOP10.

14. The transformed microorganism according to claim 12, which is the transformed *E. coli* (pTrcHis2-P) produced by introducing the recombinant expression plasmid of claim 8 or claim 10 into *E. coli* TOP 10.

15. A fused or non-fused form of NDV nucleocapsid protein isolated and purified from culture of the transformed microorganism of claim 11 or claim 13 characterised in that it has the following amino acid sequence:

1	M	S	S	V	F	D	E	Y	E	Q	L	L	A	A	Q	T	16
	ATG	TCT	TCC	GTA	TTC	GAT	GAA	TAC	GAG	CAG	CTC	CTC	GCT	GCT	CAG	ACT	
	1		10				20			30			40				
17	R	P	N	G	A	H	G	G	G	E	R	G	S	T	L	R	32
	CGC	CCC	AAT	GGA	GCT	CAC	GGA	GGG	GGA	GAG	AGA	GGG	AGC	ACT	TTA	AGA	
	50			60			70			80			90				
33	V	E	V	P	V	F	T	L	N	S	D	D	P	E	D	R	48
	GTT	GAG	GTC	CCA	GTA	TTC	ACT	CTT	AAC	AGT	GAC	GAT	CCA	GAA	GAT	AGA	
	100			110			120			130			140				
49	W	N	F	A	V	F	C	L	R	I	A	V	S	E	D	A	64
	TGG	AAT	TTT	GCG	GTA	TTC	TGT	CTT	CGG	ATT	GCT	GTT	AGC	GAG	GAC	GCC	
	150			160			170			180			190				
65	N	K	P	L	R	Q	G	A	L	I	S	L	L	C	S	H	80
	AAC	AAA	CCG	CTC	AGG	CAA	GGT	GCT	CTC	ATA	TCC	CTC	CTG	TGC	TCC	CAT	
		200				210			220		230		240				
81	S	Q	V	M	R	N	H	V	A	L	A	G	K	Q	N	E	96
	TCT	CAA	GTG	ATG	AGG	AAC	CAT	GTT	GCC	CTT	GCA	GGA	AAA	CAG	AAT	GAG	
			250			260			270				280				
97	A	T	L	T	V	L	E	I	D	G	F	T	S	S	V	P	112
	GCT	ACA	CTG	ACT	GTT	CTT	GAG	ATC	GAT	GGT	TTT	ACC	AGC	AGC	GTG	CCT	
	290		300			310			320				330				
113	Q	F	N	N	R	S	G	V	S	E	E	R	A	Q	R	F	128
	CAG	TTC	AAC	AAC	AGG	AGT	GGG	GTG	TCT	GAG	GAG	AGA	GCA	CAG	AGA	TTC	
	340			350			360			370			380				
129	M	V	I	A	G	S	L	P	R	A	C	S	N	G	T	P	144
	ATG	GTG	ATA	GCA	GGG	TCT	CTC	CCT	CGG	GGG	TGC	AGT	AAC	GGT	ACT	CCG	
		390			400		410			420			430				
145	F	V	T	A	G	V	E	D	D	A	P	E	D	I	T	D	160
	TTC	GTC	ACG	GCT	GGG	GTT	GAA	GAT	GAT	GCA	CCA	GAA	GAT	GAT	ACT	GAT	
		440			450		460			470			480				
161	T	L	E	R	I	L	S	I	Q	A	Q	V	W	V	T	V	176
	ACT	CTG	GAA	AGA	ATC	CTG	TCT	ATC	CAG	GCT	CAG	GTA	TGG	GTC	ACA	GTA	
			490			500			510			520					

5	177	A K A M T A Y E T A D E S E T R	192
		GCG AAG GCC ATG ACT GCA TAT GAG ACA GCA GAT GAG TCG GAA ACA AGA	
		530 540 550 560 570	
	193	R I N K Y M Q G R V Q K K Y I	208
		AGA ATC AAT AAG TAC ATG CAG CAA GGC AGA GTC CAG AAG AAG TAC ATC	
10		580 590 600 610 620	
	209	L H P V C R S A I Q L T I R H S	224
		CTC CAC CCT GTA TGC AGG AGT GCA ATT CAA CTC ACA ATC AGA CAT TCT	
		630 640 650 660 670	
	225	L A V R I F L V S E L K R G R N	240
15		CTG GCA GTC CGC ATT TTC TTA GTT AGC GAG CTT AAG AGA GGC CGC AAT	
		680 690 700 710 720	
	241	T A G G S S T Y Y N L V G D V D	256
		ACG GCA GGT GGG AGC TCC ACG TAT TAC AAC TTA GTA GGG GAT GTA GAC	
		730 740 750 760	
20	257	S Y I R N T G L T A F F L T L K	272
		TCA TAC ATC AGG AAC ACC GGA CTT ACT GCA TTC TTC CTT ACA CTC AAA	
		770 780 790 800 810	
	273	Y G I N T K T S A L A L S S L T	288
		TAT GGA ATT AAT ACC AAG ACA TCA GCC CTA GCA CTC AGC AGC CTC ACA	
25		820 830 840 850 860	
	289	G D I Q K M K Q L M R L Y R M K	304
		GGC GAT ATC CAA AAG ATG AAG CAG CTC ATG CGT TTA TAT CGG ATG AAG	
		870 880 890 900 910	
	305	G E N A P Y M T L L G D S D Q M	320
30		GGA GAA AAT GCG CCG TAC ATG ACA TTG CTA GGT GAC AGT GAT CAG ATG	
		920 930 940 950 960	
	321	S F A P A E Y A Q L Y S F A M G	336
		AGC TTT GCA CCG GCT GAG TAT GCA CAG CTT TAT TCT TTT GCC ATG GGC	
		970 980 990 1000	
35	337	M A S V L D K G T G K Y Q F A R	352
		ATG GCA TCA GTC TTA GAT AAA GGA ACT GGC AAA TAC CAA TTC GCC AGA	
		1010 1020 1030 1040 1050	
	353	D F M S T S F W R L G V E Y A Q	368
		GAC TTC ATG AGC ACA TCA TTC TGG AGA CTC GGG GTG GAG TAT GCT CAG	
40		1060 1070 1080 1090 1100	
	369	A Q G S S I N E D M A A E L K L	384
		GCT CAG GGG AGT AGC ATC AAC GAA GAC ATG GCT GCT GAG CTA AAA CTA	
		1110 1120 1130 1140 1150	
	385	T P A A R R G L A A A A Q R V S	400
45		ACC CCG GCA GCA AGA AGG GGC CTG GCA GGT GCT GCC CAA CGA GTG TCT	
		1160 1170 1180 1190 1200	
	401	E E T G S V D I P T Q Q A G V L	416
		GAG GAA ACT GGC AGC GTG GAT ATT CCT ACT CAA CAA GCC GGG GTC CTC	
		1210 1220 1230 1240	
50	417	T G L S D G G P R A S Q G G S N	432
		ACT GGG CTC AGC GAT GGA GGC CCC CGA GCC TCT CAG GGT GGA TCG AAC	
		1250 1260 1270 1280 1290	
	433	K S Q G Q P D A G D G E T Q F L	448
		AAG TCG CAA GGG CAA CCA GAT GCC GGA GAT GGG GAG ACC CAA TTC TTG	
		1300 1310 1320 1330 1340	

449 D L M R A V A N S M R E A P N S 464
 GAT TTG ATG AGA GCA GTG GCG AAC AGC ATG CGA GAA GCG CCA AAC TCC
 1350 1360 1370 1380 1390

5 465 A Q S T T H P E P P P T P G P S 480
 GCA CAG AGC ACC ACC CAC CCG GAA CCC CCC CCG ACT CCC GGG CCA TCC
 1400 1410 1420 1430 1440

481 Q D N D T D W G Y * 490
 CAA GAT AAC GAC ACC GAC TGG GGG TAT TGA
 1450 1460 1470

10

16. A fused or non-fused form of NDV phosphoprotein isolated and purified from culture of the transformed microorganism of claim 12 or claim 14 characterised in that it has the following amino acid sequence:

15

1 M A T F T D A E I D D I F E T S 16
 ATG GCC ACC TTT ACA GAT GCG GAG ATA GAT GAT ATA TTT GAG ACC AGT
 1 10 20 30 40

17 G T V I D S I I T A Q G K S A E 32
 GGA ACT GTC ATT GAC AGC ATA ATT ACG GCC CAG GGT AAA TCA GCA GAG
 50 60 70 80 90

20

33 T V G R S A I P Q G K T K A L S 48
 ACT GTC GGA AGG AGC GCA ATC CCA CAA GGC AAG ACC AAA GGG CTG AGC
 100 110 120 130 140

49 I A W E K H G S I Q P S T S Q D 64
 ATA GCA TGG GAG AAG CAT GGG AGC ATC CAA CCA TCC ACC AGC CAG GAC
 150 160 170 180 190

25

65 N P D Q Q D R P D K Q L S T P E 80
 AAC CCC GAC CAA CAG GAT AGA CCA CCA AAA CAG CTA TCC ACA CCT GAG
 200 210 220 230 240

30

81 Q A T P H N S S P A T S A E P L 96
 CAG GCG ACC CCA CAC AAC AGC TCG CCA GCC ACA TCC GCC GAA CCG CTC
 250 260 270 280

97 P T Q A A G E A G D T Q L K T G 112
 CCC ACT CAG GCC GCA GGT GAG GCC GGC GAC ACA CAG CTC AAG ACC GGA
 290 300 310 320 330

35

113 A S G N S L L S M L D K L S N K P 128
 GCA AGC AAC TCT CTT CTG TCT ATG CTC GAC AAG CTG AGC AAT AAA CCA
 340 350 360 370 380

129 S N A K K G P W S S P Q E G Y H 144
 TCT AAT GCT AAA AAG GGC CCA TGG TCG AGT CCC CAG GAA GGA TAT CAT
 390 400 410 420 430

40

145 Q P P T Q Q H G D Q P N R G N S 160
 CAA CCT CCG ACC CAA CAA CAT GGG GAT CAG CCG AAC CTG GGA AGC AAC GAC
 440 450 460 470 480

161 Q E R L R H Q A K A A P G S R G 176
 CAG GAG AGG CTG CGG CAC CAA GCC AAG GCC CCT GGA AGC CGG GGC
 490 500 510 520

5	177	T 530	D ACA	A GCG	S AGC	T ACA	Y TAT	H 550	G GGA	Q CAA	W TGG	K AAG	E GAG	S TCA	Q CAA	L CTA	192	
	193	S TCA	G GCT	G GGT	A GCA	T ACC	P CCT	H CAT	V GTG	L CTC	Q CAA	S TCA	G GGG	Q CAG	S AGC	Q CAA	D GAC	208
	209	S AGT	T ACT	P CCT	V GTA	P CCT	G GTG	D GAT	H CAT	V GTG	Q CAG	P CCA	P CCT	V GTC	D GAC	F TTT	V GTG	224
10	225	Q CAG	A GCG	M ATG	M ATG	T ACT	M ATG	M ATG	E GAG	A GCG	L TTA	S TCA	Q CAG	K AAG	V GTA	S AGT	A KAA	240
	241	V GTC	D GAC	Y TAT	Q CMG	L CTA	D GAC	L CTA	V GTC	L TTA	K AAG	Q CAG	T ACA	S TCC	S TCC	I ATC	P CCT	256
15	257	M 770	M ATG	R CGG	S TCT	E GAA	I ATC	Q CAA	Q CTA	L AAA	K ACA	T TCT	S VGT	S GCG	V GTC	V ATG	M ATG	272
	273	E GAA	A GCT	N AAT	L TTA	G GCG	M ATG	M ATG	K AAA	I ATT	L CTG	D GAC	P CCT	G GGT	C TGT	C GCT	N AAC	288
20	289	I ATT	S TCA	S TCC	L TTA	S AGT	D GAT	L CTG	R CGG	A GCA	V GTC	A GCC	R CGG	S TCC	H CAC	P CCA	V GTT	304
	305	L TTA	I ATT	S TCA	G GGC	P CCC	G GGA	D GAT	P COG	S TCC	P CCC	Y TAC	V GTG	T ACA	Q CAA	G GGG	G GGT	320
30	321	E GAG	M ATG	T ACA	L CTC	N AAT	K AAA	L CTC	S TCA	Q CAA	P CCA	V GTA	Q CAA	H CAC	P CCT	S TCC	E GAG	336
	337	L 1010	I ATT	K AAA	S TCT	A GCC	T ACA	A GGC	G GGC	G GGA	P CCT	D GAT	M ATG	G GGA	V GTG	E GAA	K AAG	352
35	353	D GAC	T ACT	V GTC	R CGT	A GCA	L TTG	I ATC	T ACC	S TCG	R CGC	P CCG	M ATG	H CAT	P CCA	S AGC	S TCC	368
	369	S TCA	A GCT	K AAG	L CTC	L CTG	S AGT	K AAG	L CTG	D GAT	A GCA	A GCC	G GGG	S TCG	I ATT	E GAA	E GAG	384
40	385	I ATC	R AGA	K AAG	I ATC	K AAG	R CGC	L CTT	A GCA	L CTA	N AAT	G GGC	* TAA					396